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RAW SEQUENCE LISTING   DATE: 01/04/2002
PATENT APPLICATION: US/09/662,128A   TIME: 14:47:49

Input Set : A:\197330US0.ST25.txt
Output Set: N:\CRF3\01042002\I662128A.raw

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 3 <110> APPLICANT: MIYAGAWA, SHUJI
 4        OKABE, MASARU
 6 <120> TITLE OF INVENTION: MODIFIED CRE RECOMBINASE GENE FOR MAMMALS
 8 <130> FILE REFERENCE: 197330US0
10 <140> CURRENT APPLICATION NUMBER: 09/662,128A
11 <141> CURRENT FILING DATE: 2000-09-14
13 <150> PRIOR APPLICATION NUMBER: JP11-264364
14 <151> PRIOR FILING DATE: 1999-09-17
16 <160> NUMBER OF SEQ ID NOS: 6
18 <170> SOFTWARE: PatentIn version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1050
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(1050)
29 <220> FEATURE:
30 <221> NAME/KEY: misc_feature
31 <222> LOCATION: ()..()
32 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic dna
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37 Met Pro Lys Lys Lys Arg Lys Val Ser Asn Leu Leu Thr Val His Gln
38 1               5                   10                  15
40 aac ctg ccc gcc ctg ccc gtg gac gcc acc agc gac gag gtg cgc aag       96
41 Asn Leu Pro Ala Leu Pro Val Asp Ala Thr Ser Asp Glu Val Arg Lys
42             20                  25                  30
44 aac ctg atg gac atg ttc cgc gac cgc cag gcc ttc agc gag cac acc      144
45 Asn Leu Met Asp Met Phe Arg Asp Arg Gln Ala Phe Ser Glu His Thr
46         35                  40                  45
48 tgg aag atg ctg ctg agc gtg tgc cgc agc tgg gcc gcc tgg tgc aag      192
49 Trp Lys Met Leu Leu Ser Val Cys Arg Ser Trp Ala Ala Trp Cys Lys
50      50                  55                  60
52 ctg aac aac cgc aag tgg ttc ccc gcc gag ccc gag gac gtg cgc gac      240
53 Leu Asn Asn Arg Lys Trp Phe Pro Ala Glu Pro Glu Asp Val Arg Asp
54 65                  70                  75                  80
56 tac ctg ctg tac ctg cag gcc cgc ggc ctg gcc gtg aag acc atc cag      288
57 Tyr Leu Leu Tyr Leu Gln Ala Arg Gly Leu Ala Val Lys Thr Ile Gln
58                  85                  90                  95
60 cag cac ctg ggc cag ctg aac atg ctg cac cgc cgc agc ggc ctg ccc      336
61 Gln His Leu Gly Gln Leu Asn Met Leu His Arg Arg Ser Gly Leu Pro
62             100                 105                 110
64 cgc ccc agc gac agc aac gcc gtg agc ctg gtg atg cgc cgc atc cgc      384
65 Arg Pro Ser Asp Ser Asn Ala Val Ser Leu Val Met Arg Arg Ile Arg
66             115                 120                 125
68 aag gag aac gtg gac gcc ggc gag cgc gcc aag cag gcc ctg gcc ttc      432
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69 Lys Glu Asn Val Asp Ala Gly Glu Arg Ala Lys Gln Ala Leu Ala Phe
70       130                 135                 140
72 gag cgc acc gac ttc gac cag gtg cgc agc ctg atg gag aac agc gac       480
73 Glu Arg Thr Asp Phe Asp Gln Val Arg Ser Leu Met Glu Asn Ser Asp
74 145                 150                 155                 160
76 cgc tgc cag gac atc cgc aac ctg gcc ttc ctg ggc atc gcc tac aac       528
77 Arg Cys Gln Asp Ile Arg Asn Leu Ala Phe Leu Gly Ile Ala Tyr Asn
78                 165                 170                 175
80 acc ctg ctg cgc atc gcc gag atc gcc cgc atc cgc gtg aag gac atc       576
81 Thr Leu Leu Arg Ile Ala Glu Ile Ala Arg Ile Arg Val Lys Asp Ile
82                 180                 185                 190
84 agc cgc acc gac ggc ggc cgc atg ctg atc cac atc ggc cgc acc aag       624
85 Ser Arg Thr Asp Gly Gly Arg Met Leu Ile His Ile Gly Arg Thr Lys
86           195                 200                 205
88 acc ctg gtg agc acc gcc ggc gtg gag aag gcc ctg agc ctg ggc gtg       672
89 Thr Leu Val Ser Thr Ala Gly Val Glu Lys Ala Leu Ser Leu Gly Val
90       210                 215                 220
92 acc aag ctg gtg gag cgc tgg atc agc gtg agc ggc gtg gcc gac gac       720
93 Thr Lys Leu Val Glu Arg Trp Ile Ser Val Ser Gly Val Ala Asp Asp
94 225                 230                 235                 240
96 ccc aac aac tac ctg ttc tgc cgc gtg cgc aag aac ggc gtg gcc gcc       768
97 Pro Asn Asn Tyr Leu Phe Cys Arg Val Arg Lys Asn Gly Val Ala Ala
98                 245                 250                 255
100 ccc agc gcc acc agc cag ctg agc acc cgg gcc ctg gag ggc atc ttc      816
101 Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg Ala Leu Glu Gly Ile Phe
102               260                 265                 270
104 gag gcc acc cac cgc ctg atc tac ggc gcc aag gac gac agc ggc cag      864
105 Glu Ala Thr His Arg Leu Ile Tyr Gly Ala Lys Asp Asp Ser Gly Gln
106           275                 280                 285
108 cgc tac ctg gcc tgg agc ggc cac agc gcc cgc gtg ggc gcc gcc cgc      912
109 Arg Tyr Leu Ala Trp Ser Gly His Ser Ala Arg Val Gly Ala Ala Arg
110       290                 295                 300
112 gac atg gcc cgc gcc ggc gtg agc atc ccc gag atc atg cag gcc ggc      960
113 Asp Met Ala Arg Ala Gly Val Ser Ile Pro Glu Ile Met Gln Ala Gly
114 305                 310                 315                 320
116 ggc tgg acc aac gtg aac atc gtg atg aac tac atc cgc aac ctg gac      1008
117 Gly Trp Thr Asn Val Asn Ile Val Met Asn Tyr Ile Arg Asn Leu Asp
118                 325                 330                 335
120 agc gag acc ggc gcc atg gtg cgc ctg ctg gag gac ggc gac           1050
121 Ser Glu Thr Gly Ala Met Val Arg Leu Leu Glu Asp Gly Asp
122           340                 345                 350
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126 <211> LENGTH: 350
127 <212> TYPE: PRT
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131 <221> NAME/KEY: misc_feature
132 <222> LOCATION: ()..()
133 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
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141 Asn Leu Pro Ala Leu Pro Val Asp Ala Thr Ser Asp Glu Val Arg Lys
142              20                  25                  30
145 Asn Leu Met Asp Met Phe Arg Asp Arg Gln Ala Phe Ser Glu His Thr
146          35                  40                  45
149 Trp Lys Met Leu Leu Ser Val Cys Arg Ser Trp Ala Ala Trp Cys Lys
150      50                  55                  60
153 Leu Asn Asn Arg Lys Trp Phe Pro Ala Glu Pro Glu Asp Val Arg Asp
154 65                  70                  75                  80
157 Tyr Leu Leu Tyr Leu Gln Ala Arg Gly Leu Ala Val Lys Thr Ile Gln
158              85                  90                  95
161 Gln His Leu Gly Gln Leu Asn Met Leu His Arg Arg Ser Gly Leu Pro
162          100                 105                 110
165 Arg Pro Ser Asp Ser Asn Ala Val Ser Leu Val Met Arg Arg Ile Arg
166          115                 120                 125
169 Lys Glu Asn Val Asp Ala Gly Glu Arg Ala Lys Gln Ala Leu Ala Phe
170      130                 135                 140
173 Glu Arg Thr Asp Phe Asp Gln Val Arg Ser Leu Met Glu Asn Ser Asp
174 145                 150                 155                 160
177 Arg Cys Gln Asp Ile Arg Asn Leu Ala Phe Leu Gly Ile Ala Tyr Asn
178              165                 170                 175
181 Thr Leu Leu Arg Ile Ala Glu Ile Ala Arg Ile Arg Val Lys Asp Ile
182              180                 185                 190
185 Ser Arg Thr Asp Gly Gly Arg Met Leu Ile His Ile Gly Arg Thr Lys
186          195                 200                 205
189 Thr Leu Val Ser Thr Ala Gly Val Glu Lys Ala Leu Ser Leu Gly Val
190      210                 215                 220
193 Thr Lys Leu Val Glu Arg Trp Ile Ser Val Ser Gly Val Ala Asp Asp
194 225                 230                 235                 240
197 Pro Asn Asn Tyr Leu Phe Cys Arg Val Arg Lys Asn Gly Val Ala Ala
198              245                 250                 255
201 Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg Ala Leu Glu Gly Ile Phe
202          260                 265                 270
205 Glu Ala Thr His Arg Leu Ile Tyr Gly Ala Lys Asp Asp Ser Gly Gln
206          275                 280                 285
209 Arg Tyr Leu Ala Trp Ser Gly His Ser Ala Arg Val Gly Ala Ala Arg
210      290                 295                 300
213 Asp Met Ala Arg Ala Gly Val Ser Ile Pro Glu Ile Met Gln Ala Gly
214 305                 310                 315                 320
217 Gly Trp Thr Asn Val Asn Ile Val Met Asn Tyr Ile Arg Asn Leu Asp
218              325                 330                 335
221 Ser Glu Thr Gly Ala Met Val Arg Leu Leu Glu Asp Gly Asp
222          340                 345                 350
225 <210> SEQ ID NO: 3
226 <211> LENGTH: 34
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
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230 <220> FEATURE:
231 <221> NAME/KEY: misc_feature
232 <222> LOCATION: ()..()
233 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
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241 <211> LENGTH: 29
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <221> NAME/KEY: misc_feature
247 <222> LOCATION: ()..()
248 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
251 <400> SEQUENCE: 4
252 ttcgtatagc atagattata cgaagttat                                  29
255 <210> SEQ ID NO: 5
256 <211> LENGTH: 29
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <221> NAME/KEY: misc_feature
262 <222> LOCATION: ()..()
263 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
266 <400> SEQUENCE: 5
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271 <211> LENGTH: 21
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <221> NAME/KEY: misc_feature
277 <222> LOCATION: ()..()
278 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
281 <400> SEQUENCE: 6
282 cccaagaaga agaggaaggt g                                          21
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VERIFICATION SUMMARY   DATE: 01/04/2002
PATENT APPLICATION: US/09/662,128A   TIME: 14:47:50

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